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SEQUENCE LISTING

<110> Neurotech Pharmaceuticals Co., Ltd.
Han, Pyung Lim
Lee, Kang-Woo
Yang, Sung-Don
Song, Jin-Sook

<120> TRANSGENIC MICE INDUCING ALZHEIMER'S
DISEASE EXPRESSING MUTANT BETACTF99

<130> 11281-118-999

<140> To be Assigned
<141> 2006-09-20

<150> KR 10-2004-0022562
<151> 2004-04-01

<160> 25

<170> FastSEQ for Windows Version 4.0

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<211> 3148
<212> DNA
<213> Homo sapiens

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 <211> 751
 <212> PRT
 <213> Homo sapiens

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 Gln Ile Ala Met Phe Cys Gly Arg Leu Asn Met His Met Asn Val Gln
 35 40 45
 Asn Gly Lys Trp Asp Ser Asp Pro Ser Gly Thr Lys Thr Cys Ile Asp
 50 55 60
 Thr Lys Glu Gly Ile Leu Gln Tyr Cys Gln Glu Val Tyr Pro Glu Leu
 65 70 75 80
 Gln Ile Thr Asn Val Val Glu Ala Asn Gln Pro Val Thr Ile Gln Asn
 85 90 95
 Trp Cys Lys Arg Gly Arg Lys Gln Cys Lys Thr His Pro His Phe Val
 100 105 110
 Ile Pro Tyr Arg Cys Leu Val Gly Glu Phe Val Ser Asp Ala Leu Leu
 115 120 125
 Val Pro Asp Lys Cys Lys Phe Leu His Gln Glu Arg Met Asp Val Cys
 130 135 140
 Glu Thr His Leu His Trp His Thr Val Ala Lys Glu Thr Cys Ser Glu
 145 150 155 160
 Lys Ser Thr Asn Leu His Asp Tyr Gly Met Leu Leu Pro Cys Gly Ile
 165 170 175
 Asp Lys Phe Arg Gly Val Glu Phe Val Cys Cys Pro Leu Ala Glu Glu
 180 185 190

Ser Asp Asn Val Asp Ser Ala Asp Ala Glu Glu Asp Asp Ser Asp Val
195 200 205
Trp Trp Gly Gly Ala Asp Thr Asp Tyr Ala Asp Gly Ser Glu Asp Lys
210 215 220
Val Val Glu Val Ala Glu Glu Glu Val Ala Glu Val Glu Glu Glu
225 230 235 240
Glu Ala Asp Asp Asp Glu Asp Asp Glu Asp Gly Asp Glu Val Glu Glu
245 250 255
Glu Ala Glu Glu Pro Tyr Glu Glu Ala Thr Glu Arg Thr Thr Ser Ile
260 265 270
Ala Thr Thr Thr Thr Thr Glu Ser Val Glu Glu Val Val Arg
275 280 285
Glu Val Cys Ser Glu Gln Ala Glu Thr Gly Pro Cys Arg Ala Met Ile
290 295 300
Ser Arg Trp Tyr Phe Asp Val Thr Glu Gly Lys Cys Ala Pro Phe Phe
305 310 315 320
Tyr Gly Gly Cys Gly Gly Asn Arg Asn Asn Phe Asp Thr Glu Glu Tyr
325 330 335
Cys Met Ala Val Cys Gly Ser Ala Ile Pro Thr Thr Ala Ala Ser Thr
340 345 350
Pro Asp Ala Val Asp Lys Tyr Leu Glu Thr Pro Gly Asp Glu Asn Glu
355 360 365
His Ala His Phe Gln Lys Ala Lys Glu Arg Leu Glu Ala Lys His Arg
370 375 380
Glu Arg Met Ser Gln Val Met Arg Glu Trp Glu Glu Ala Glu Arg Gln
385 390 395 400
Ala Lys Asn Leu Pro Lys Ala Asp Lys Lys Ala Val Ile Gln His Phe
405 410 415
Gln Glu Lys Val Glu Ser Leu Glu Gln Glu Ala Ala Asn Glu Arg Gln
420 425 430
Gln Leu Val Glu Thr His Met Ala Arg Val Glu Ala Met Leu Asn Asp
435 440 445
Arg Arg Arg Leu Ala Leu Glu Asn Tyr Ile Thr Ala Leu Gln Ala Val
450 455 460
Pro Pro Arg Pro Arg His Val Phe Asn Met Leu Lys Lys Tyr Val Arg
465 470 475 480
Ala Glu Gln Lys Asp Arg Gln His Thr Leu Lys His Phe Glu His Val
485 490 495
Arg Met Val Asp Pro Lys Lys Ala Ala Gln Ile Arg Ser Gln Val Met
500 505 510
Thr His Leu Arg Val Ile Tyr Glu Arg Met Asn Gln Ser Leu Ser Leu
515 520 525
Leu Tyr Asn Val Pro Ala Val Ala Glu Glu Ile Gln Asp Glu Val Asp
530 535 540
Glu Leu Leu Gln Lys Glu Gln Asn Tyr Ser Asp Asp Val Leu Ala Asn
545 550 555 560
Met Ile Ser Glu Pro Arg Ile Ser Tyr Gly Asn Asp Ala Leu Met Pro
565 570 575
Ser Leu Thr Glu Thr Lys Thr Val Glu Leu Leu Pro Val Asn Gly
580 585 590
Glu Phe Ser Leu Asp Asp Leu Gln Pro Trp His Ser Phe Gly Ala Asp
595 600 605
Ser Val Pro Ala Asn Thr Glu Asn Glu Val Glu Pro Val Asp Ala Arg
610 615 620
Pro Ala Ala Asp Arg Gly Leu Thr Thr Arg Pro Gly Ser Gly Leu Thr
625 630 635 640
Asn Ile Lys Thr Glu Glu Ile Ser Glu Val Lys Met Asp Ala Glu Phe

645	650	655
Arg His Asp Ser Gly Tyr Glu Val His His Gln Lys Leu Val Phe Phe		
660	665	670
Ala Glu Asp Val Gly Ser Asn Lys Gly Ala Ile Ile Gly Leu Met Val		
675	680	685
Gly Gly Val Val Ile Ala Thr Val Ile Val Ile Thr Leu Val Met Leu		
690	695	700
Lys Lys Lys Gln Tyr Thr Ser Ile His His Gly Val Val Glu Val Asp		
705	710	715
Ala Ala Val Thr Pro Glu Glu Arg His Leu Ser Lys Met Gln Gln Asn		
725	730	735
Gly Tyr Glu Asn Pro Thr Tyr Lys Phe Phe Glu Gln Met Gln Asn		
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 <212> DNA
 <213> Artificial Sequence

<220>
 <223> C-terminal fragment of APP bearing V717F mutation

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 ctgaacatgc acatgaatgt ccagaatggg aagtgggatt cagatccatc agggaccaaa 180
 acctgcattt ataccaagga aggcatcctg cagtattgcc aagaagtctt ccctgaactg 240
 cagatcacca atgtggtaga agccaaccaa ccagtgcacca tccagaactg gtgcacgg 300
 ggcgcgaagc agtgcacccac ccattccccac tttgtgattt cctaccgcgtt cttagtttgt 360
 gagtttgtaa gtgatgcctt tctcggttccct gacaagtgc aattcttaca ccagggagg 420
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 aagagtacca acttgcacca ctacggcatg ttgctgcctt gcggaatttgc caagttccga 540
 gggtagagt ttgtgtgttgc cccactggctt gaagaaagtgc acaatgttgc ttctgctgtat 600
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 gaagccgatg atgacgaggat ggtgatgggg tagaggaaga ggctgaggaa 780
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 tacggcggat gtggcgccaa ccggaaacaaac tttgacacag aagagtactg catggccgtg 1020
 tgtggcagcg ccattccctac aacagcagcc agtaccctgtt atgcccgttgc caagtatctc 1080
 gagacacctg gggatgagaa tgaacatgcc cattttccaga aagccaaaga gaggcttgag 1140
 gccaaggcacc gagagagaat gtcccagggtc atgagagaat gggaaagagc agaacgtcaa 1200
 gcaaaagaact tgcctaaagc tgataagaag gcagttatcc agcatttcca ggagaaagtgg 1260
 gaatctttgg aacaggaagc agccaacggc agacagcagc tgggtggagac acacatggcc 1320
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 gcagaacaga aggacagaca gcacacccta aagcatttgc agcatgtgcg catggtgat 1500
 cccaagaaag ccgctcagat ccgggtcccaag gttatgacac acctccgtgtt gatttttgag 1560
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<211> 770
<212> PRT
<213> Homo sapiens

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35 40 45
Asn Gly Lys Trp Asp Ser Asp Pro Ser Gly Thr Lys Thr Cys Ile Asp
50 55 60
Thr Lys Glu Gly Ile Leu Gln Tyr Cys Gln Glu Val Tyr Pro Glu Leu
65 70 75 80
Gln Ile Thr Asn Val Val Glu Ala Asn Gln Pro Val Thr Ile Gln Asn
85 90 95
Trp Cys Lys Arg Gly Arg Lys Gln Cys Lys Thr His Pro His Phe Val
100 105 110
Ile Pro Tyr Arg Cys Leu Val Gly Glu Phe Val Ser Asp Ala Leu Leu
115 120 125
Val Pro Asp Lys Cys Lys Phe Leu His Gln Glu Arg Met Asp Val Cys
130 135 140
Glu Thr His Leu His Trp His Thr Val Ala Lys Glu Thr Cys Ser Glu
145 150 155 160
Lys Ser Thr Asn Leu His Asp Tyr Gly Met Leu Leu Pro Cys Gly Ile
165 170 175
Asp Lys Phe Arg Gly Val Glu Phe Val Cys Cys Pro Leu Ala Glu Glu
180 185 190
Ser Asp Asn Val Asp Ser Ala Asp Ala Glu Glu Asp Asp Ser Asp Val
195 200 205
Trp Trp Gly Gly Ala Asp Thr Asp Tyr Ala Asp Gly Ser Glu Asp Lys
210 215 220
Val Val Glu Val Ala Glu Glu Glu Val Ala Glu Val Glu Glu Glu
225 230 235 240
Glu Ala Asp Asp Asp Glu Asp Asp Glu Asp Gly Asp Glu Val Glu Glu
245 250 255
Glu Ala Glu Glu Pro Tyr Glu Glu Ala Thr Glu Arg Thr Thr Ser Ile
260 265 270
Ala Thr Thr Thr Thr Thr Glu Ser Val Glu Glu Val Val Val Arg
275 280 285
Glu Val Cys Ser Glu Gln Ala Glu Thr Gly Pro Cys Arg Ala Met Ile
290 295 300
Ser Arg Trp Tyr Phe Asp Val Thr Glu Gly Lys Cys Ala Pro Phe Phe
305 310 315 320
Tyr Gly Gly Cys Gly Gly Asn Arg Asn Asn Phe Asp Thr Glu Glu Tyr
325 330 335
Cys Met Ala Val Cys Gly Ser Ala Met Ser Gln Ser Leu Leu Lys Thr
340 345 350
Thr Gln Glu Pro Leu Ala Arg Asp Pro Val Lys Leu Pro Thr Thr Ala

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Glu Asn Glu His Ala His Phe Gln Lys Ala Lys Glu Arg Leu Glu Ala		
385	390	395
Lys His Arg Glu Arg Met Ser Gln Val Met Arg Glu Trp Glu Glu Ala		
405	410	415
Glu Arg Gln Ala Lys Asn Leu Pro Lys Ala Asp Lys Lys Ala Val Ile		
420	425	430
Gln His Phe Gln Glu Lys Val Glu Ser Leu Glu Gln Glu Ala Ala Asn		
435	440	445
Glu Arg Gln Gln Leu Val Glu Thr His Met Ala Arg Val Glu Ala Met		
450	455	460
Leu Asn Asp Arg Arg Arg Leu Ala Leu Glu Asn Tyr Ile Thr Ala Leu		
465	470	475
Gln Ala Val Pro Pro Arg Pro Arg His Val Phe Asn Met Leu Lys Lys		
485	490	495
Tyr Val Arg Ala Glu Gln Lys Asp Arg Gln His Thr Leu Lys His Phe		
500	505	510
Glu His Val Arg Met Val Asp Pro Lys Lys Ala Ala Gln Ile Arg Ser		
515	520	525
Gln Val Met Thr His Leu Arg Val Ile Tyr Glu Arg Met Asn Gln Ser		
530	535	540
Leu Ser Leu Leu Tyr Asn Val Pro Ala Val Ala Glu Glu Ile Gln Asp		
545	550	555
Glu Val Asp Glu Leu Leu Gln Lys Glu Gln Asn Tyr Ser Asp Asp Val		
565	570	575
Leu Ala Asn Met Ile Ser Glu Pro Arg Ile Ser Tyr Gly Asn Asp Ala		
580	585	590
Leu Met Pro Ser Leu Thr Glu Thr Lys Thr Val Glu Leu Leu Pro		
595	600	605
Val Asn Gly Glu Phe Ser Leu Asp Asp Leu Gln Pro Trp His Ser Phe		
610	615	620
Gly Ala Asp Ser Val Pro Ala Asn Thr Glu Asn Glu Val Glu Pro Val		
625	630	635
Asp Ala Arg Pro Ala Ala Asp Arg Gly Leu Thr Thr Arg Pro Gly Ser		
645	650	655
Gly Leu Thr Asn Ile Lys Thr Glu Glu Ile Ser Glu Val Lys Met Asp		
660	665	670
Ala Glu Phe Arg His Asp Ser Gly Tyr Glu Val His His Gln Lys Leu		
675	680	685
Val Phe Phe Ala Glu Asp Val Gly Ser Asn Lys Gly Ala Ile Ile Gly		
690	695	700
Leu Met Val Gly Gly Val Val Ile Ala Thr Val Ile Val Ile Thr Leu		
705	710	715
Val Met Leu Lys Lys Gln Tyr Thr Ser Ile His His Gly Val Val		
725	730	735
Glu Val Asp Ala Ala Val Thr Pro Glu Glu Arg His Leu Ser Lys Met		
740	745	750
Gln Gln Asn Gly Tyr Glu Asn Pro Thr Tyr Lys Phe Phe Glu Gln Met		
755	760	765
Gln Asn		
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<211> 300

<212> DNA
<213> Artificial Sequence

<220>
<223> mutant gene bCTF99(V717F)

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gcagaagatg tgggttcaaa caaaggtgca atcattggac tcatgggtgg cggtgttg 120
atagcgacag tgatcttcat caccctggtg atgctgaaga agaaaacagta cacatccatt 180
catcatggtg tggtggaggt tgacgcccgt gtcaccccg aggagcgcca cctgtccaag 240
atgcagcaga acggctacga aaatccaacc tacaagttct ttgagcagat gcagaactag 300

<210> 6
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> app-1f primer

<400> 6
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<210> 7
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> app-1r primer

<400> 7
gggggactag ttctgcacatc gctc 24

<210> 8
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> app-2f primer

<400> 8
cctacaacag cagccagtagcc 25

<210> 9
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> app-2r primer

<400> 9
gacattctct ctcggtgctt ggcc 24

<210> 10
<211> 99
<212> PRT
<213> Artificial Sequence

<220>
<223> polypeptide encoded by mutant gene bCTF99(V717F)

<400> 10
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20 25 30
Gly Leu Met Val Gly Gly Val Val Ile Ala Thr Val Ile Phe Ile Thr
35 40 45
Leu Val Met Leu Lys Lys Lys Gln Tyr Thr Ser Ile His His Gly Val
50 55 60
Val Glu Val Asp Ala Ala Val Thr Pro Glu Glu Arg His Leu Ser Lys
65 70 75 80
Met Gln Gln Asn Gly Tyr Glu Asn Pro Thr Tyr Lys Phe Phe Glu Gln
85 90 95
Met Gln Asn

<210> 11
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> app-717-r primer

<400> 11
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<210> 12
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<212> DNA
<213> Artificial Sequence

<220>
<223> app-717-f primer

<400> 12
gcgacagtga tcttcatcac cttg 24

<210> 13
<211> 33
<212> DNA
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<220>
<223> SV40pA-f primer

<400> 13

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<210> 14	
<211> 32	
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<400> 15	
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<210> 19
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<212> DNA
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<220>
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<223> trint-f1 primer

<400> 20
aatgtatcat gcctcttgc acc 23

<210> 21
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<220>
<223> app-koz-r primer

<400> 21
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<210> 22
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<212> DNA
<213> Artificial Sequence

<220>
<223> app-sig-1f primer

<400> 22
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<210> 23
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> app-sig-1r primer

<400> 23
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<210> 24
<211> 20

<212> DNA
<213> Artificial Sequence

<220>
<223> app99f primer

<400> 24
cgaattcgat gcagaattcc 20

<210> 25
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> sequence encoding APP signal peptide

<400> 25
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